

FIG. 1

GENETIC MARKERS, STSs,  
 AND RECOMBINANTS

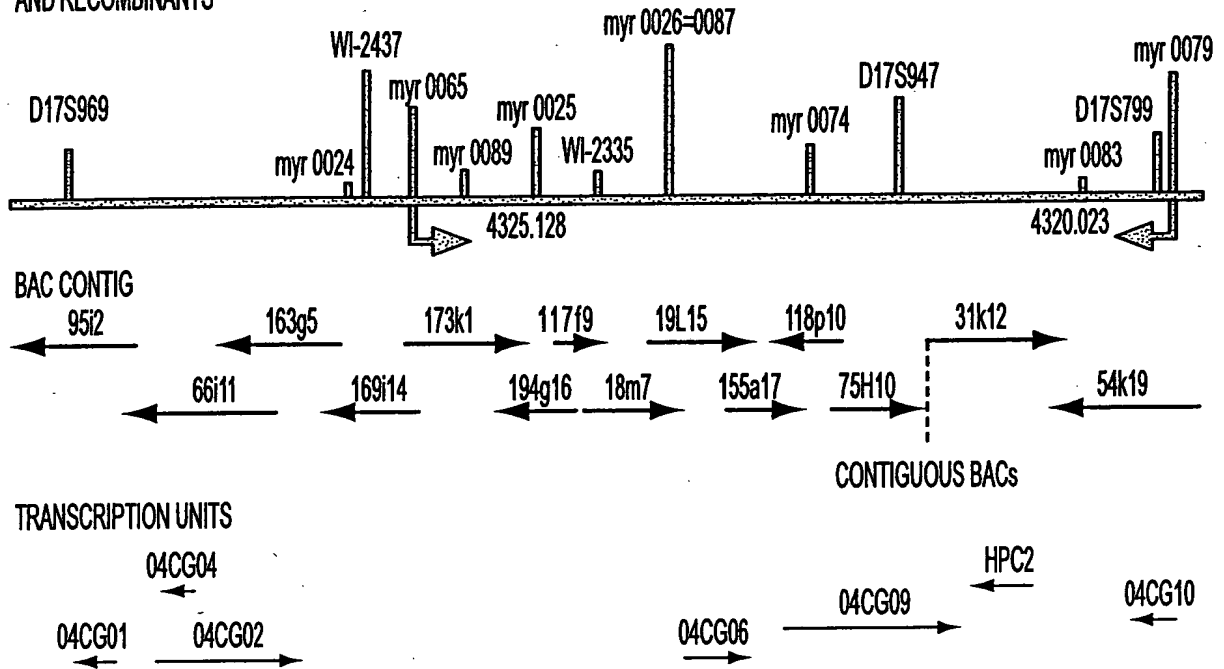


FIG. 2A

BAC 31k12 WITH 2 EXONS OF 04CG09 AND THE HPC2 TRANSCRIPTION UNIT

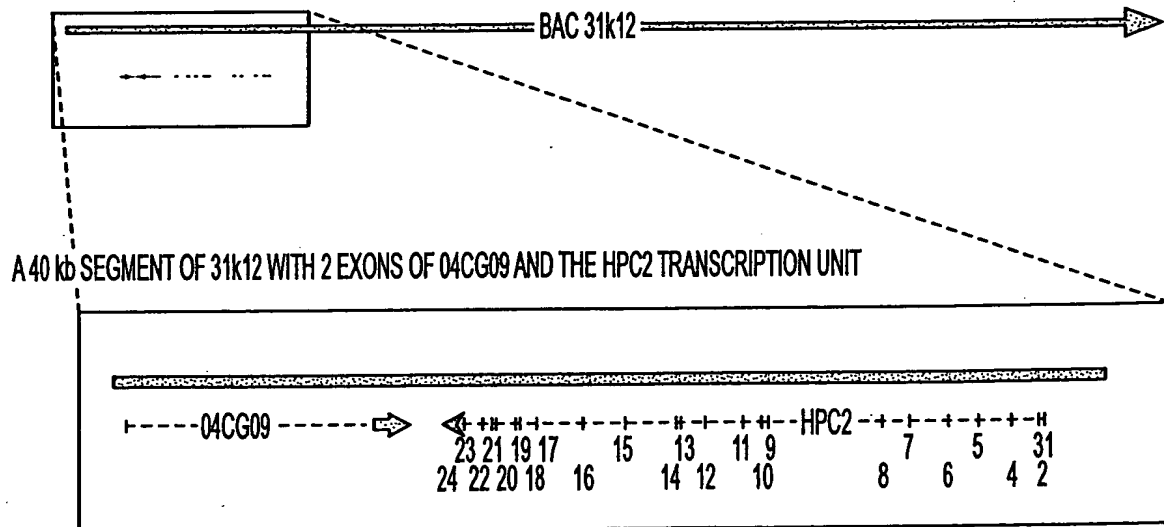


FIG. 2B

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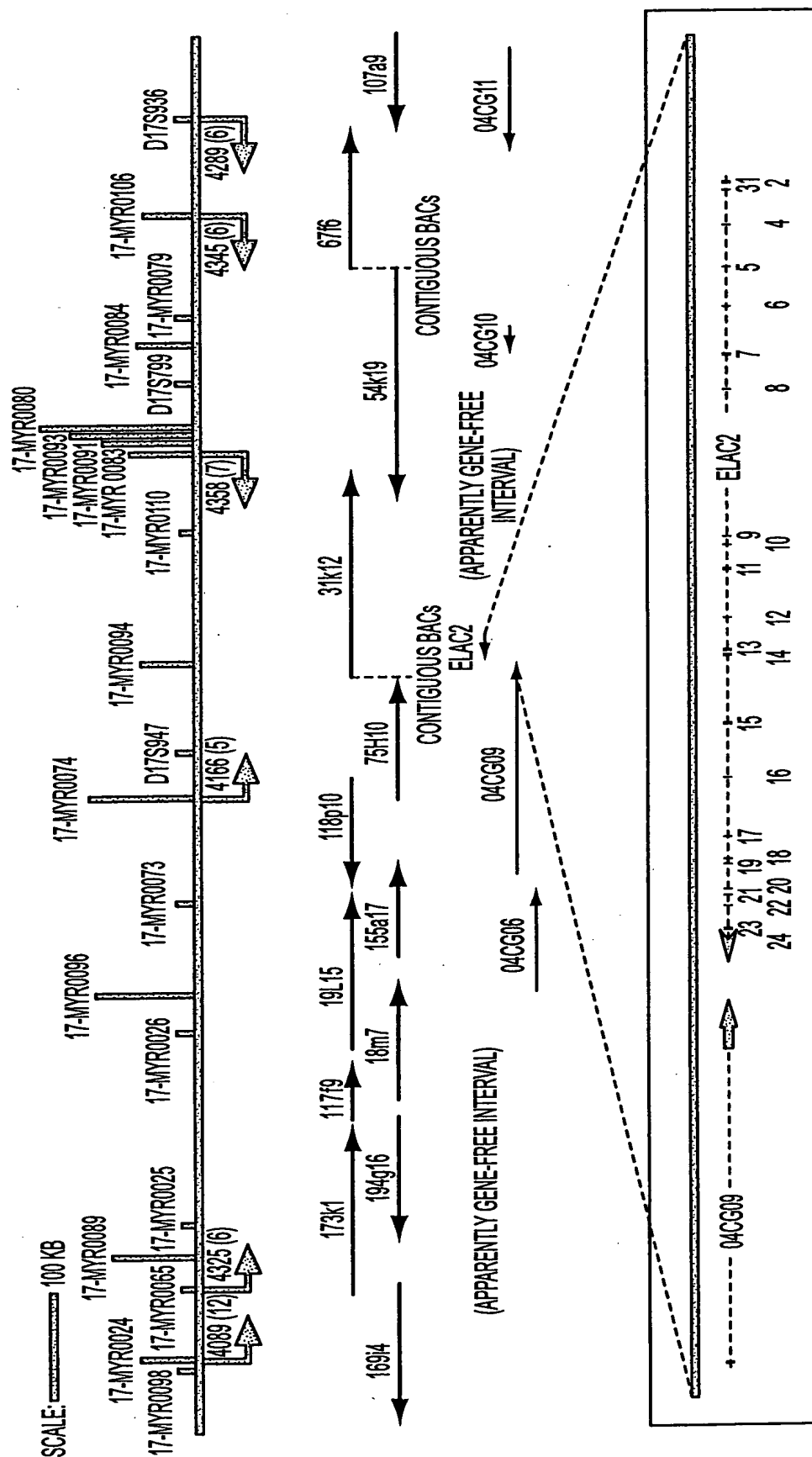


FIG. 3

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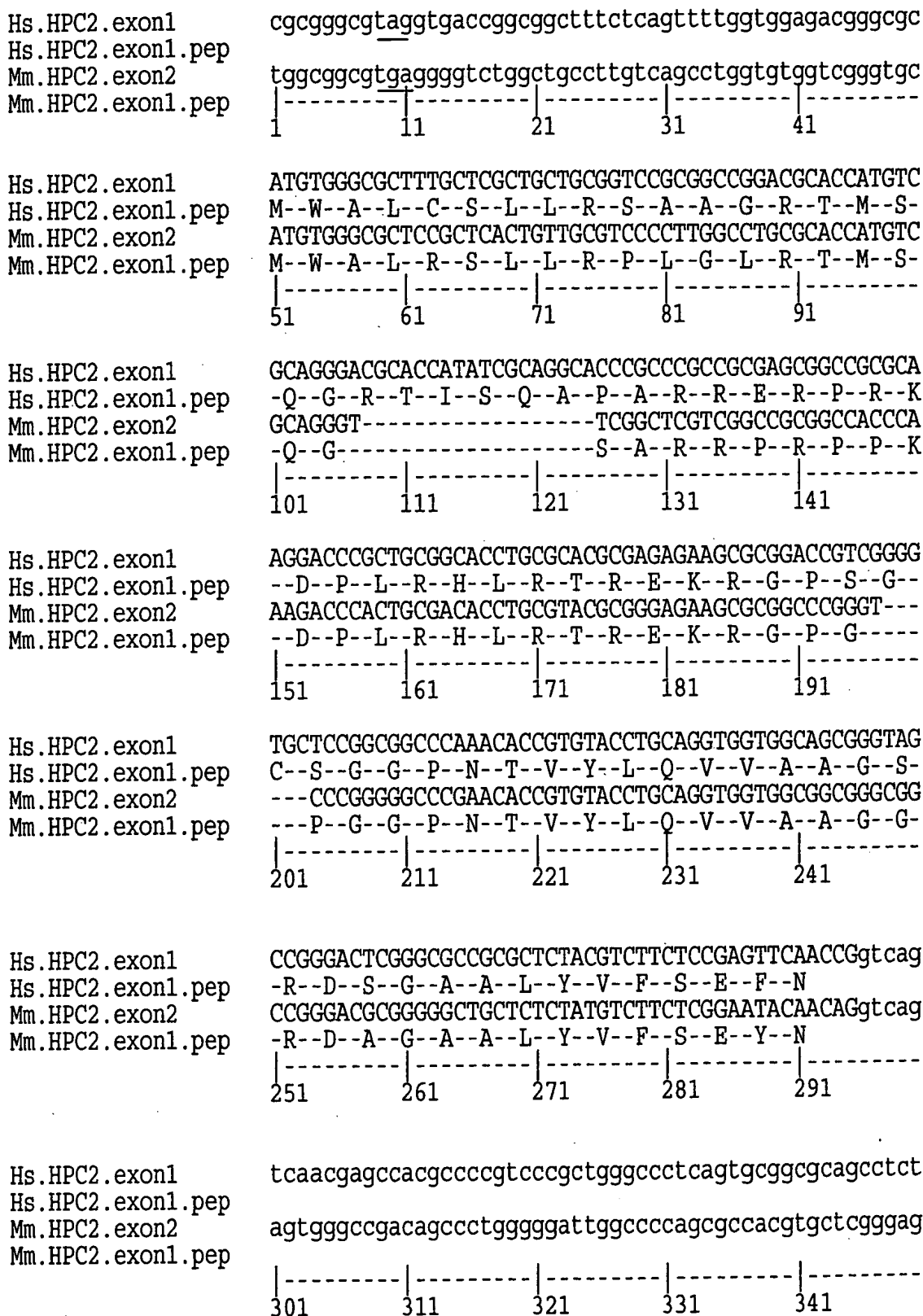
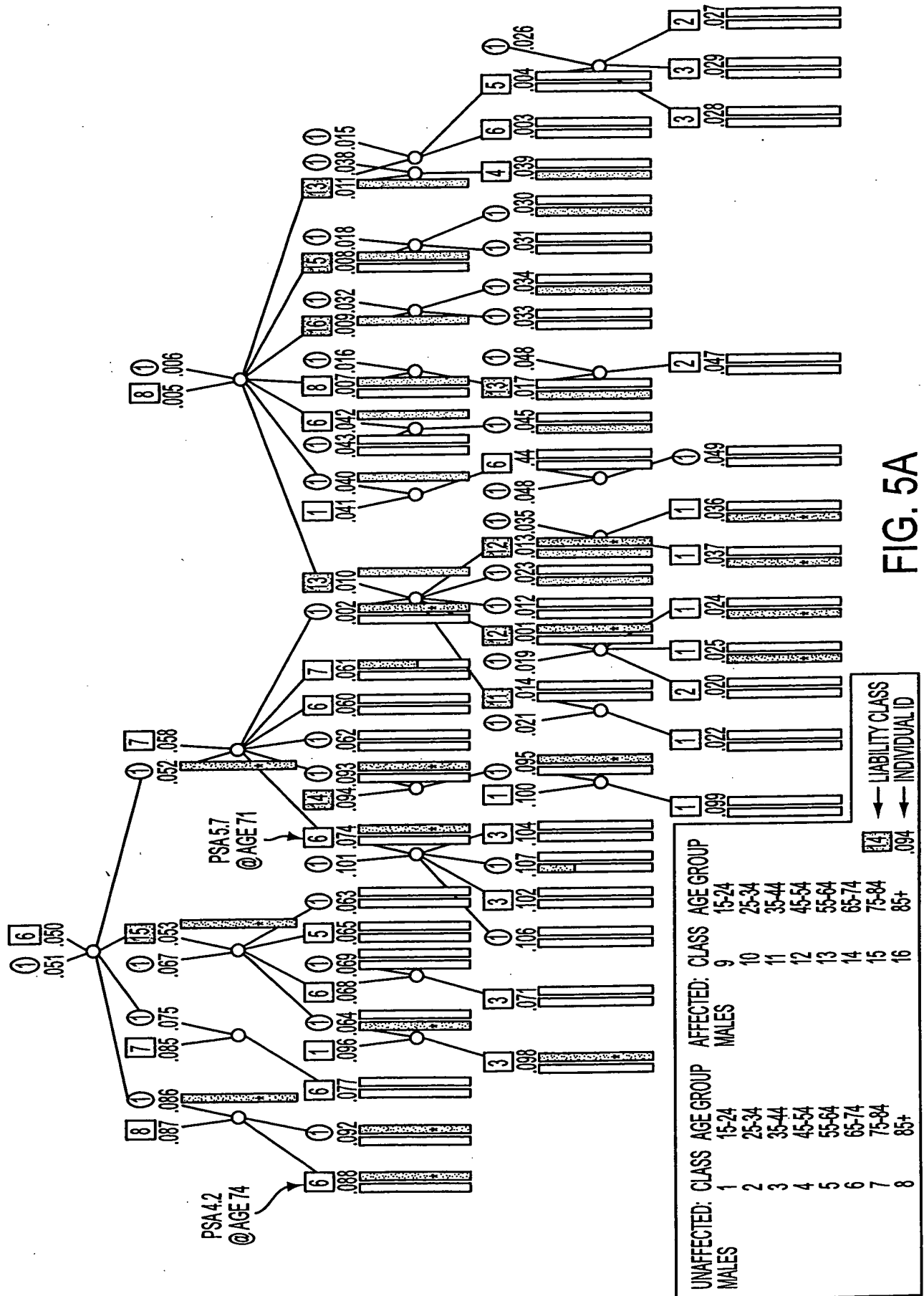


FIG. 4

FIG. 5A



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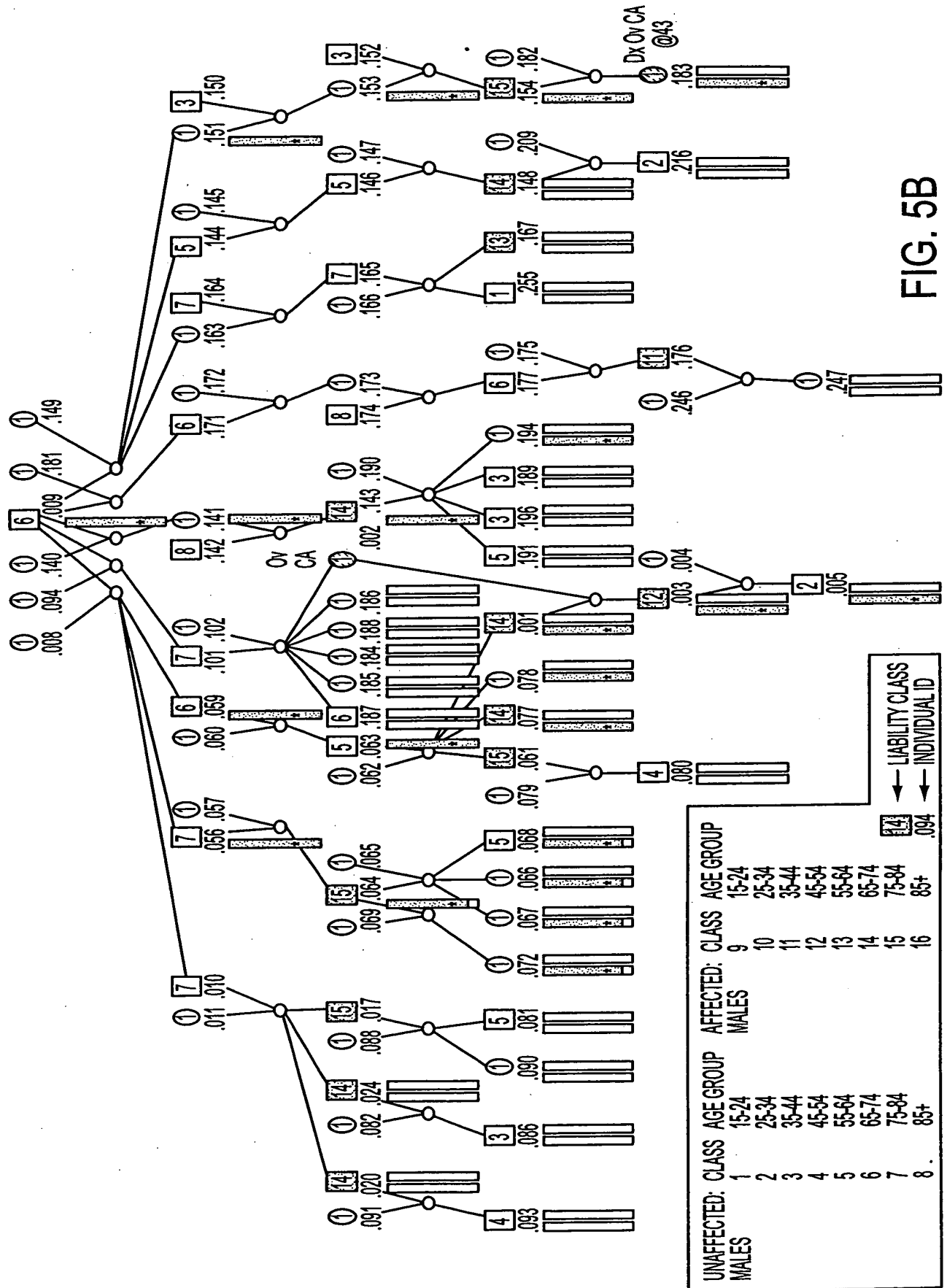


FIG. 5B

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(HSA) ELAC2	1	MWALCSLLRSAAAGRTNSQRTISQAPARPRPRKDLHLRTRKRGPSGSGGPNVYLQWVA
(MMU) Elac2	1	MWALRSLLPLGLRTMSQ.....SARPRPSKDLHLRTRKRG.....GPGGPNVYLQWVA
(CEL) CE16965	1	1 MXMLFPGIKVSRHLISSTCLFKDNNBELLESIKERIAARRRILQVHSSSHLKAREVNASISNLQSMMAVQKQKAAHEPPANS·IVNIPSVQSVIEVLG
(ATH) gi6850339	1	MENNEATNGSKSSSSNVFNKRAAGFDITDKKRNLERKSQK·LNPTNTIYAAQILG
(SCE) YKR079C	1	MPTFLPPTH
(HSA) ELAC2	65	AGSRDGAALVYFSEFNR·YLPNCGEGVQRLNQEHKLVARLDNLT·RMHWSNVGSGSMILLKTKETGLPK·CVLSGPPQLKXVL·EALNIF.....
(MMU) Elac2	57	AGGRDAGAALVYFSEYNR·YLPNCGEGVQRLNQEHKLVARLDNLT·RMHWSNVGSGSMILLKTKETGLPK·CVLSGPPQLKXVL·EALNIF.....
(CEL) CE16965	100	N·GTGLLRACFLRLTPLKT·YMPNCPENACRFLWLQIRIRSSVVDLFTT·SANDNIAIAGTSSILLIS·KESNALS·TRLHGAMNKHFL·ECTRPFDQSD
(ATH) gi6850339	58	TGMDTDTSSVLLFPDKQRFIPNAGGLQRFCTEHKIKLSKIDVFLS·RWCSETAGGUPGLLLTAGIGBEGLSVNVWGPSDLNVLV·DAMNSFIPIRA
(SCE) YKR079C	10	PTSDFKHPLLLWQSAHGEKVEFGKIFGSGQSRLTENKIRISKLKDIFLTGELNWSDI·GCHPGLMILLADQGXSN·LVHLYGNDILNVLIVSTWRYVVRFR
(HSA) ELAC2	155	.....SGPLK·GIELAVR.....PHSAPEYDETMVYQIPIHSEQRGRKHQWPQSPRPLSRLSEFSSDSSESNENPHLP..
(MMU) Elac2	147	.....SGPLK·GIELAVR.....PHSAPEYDETMVYQVPIHSERRCGKQOPSQSPRTSPNRLSPKQSSDGSSEN·GOCPE
(CEL) CE16965	193	.....YGCKY·PSQVEER.....PITMENYEDAGLKVTYP.....LSP·PLNIGSNNEKS.....
(ATH) gi6850339	156	AMVHTRSGPSSPDPIVLVNDDEVKISAIL.....LXP·CHSBEEDSGNKGSD.....
(SCE) YKR079C	108	.....GIDENDHMKDREYKDKLIAVKSFNKNGGDRLEVPDPSQKGLRSIVA.....KMPPKHAPTDTRYDPSDPLN.....
(HSA) ELAC2	226	..HGVSQRGV·RDSLSVVAITCNHLKRGNFLLVKAKENGEPVGTAAIAPITIAAVKDGKSTT·HEGEFILAEECTP.....PDPGAAPFWWVECP·DESF
(MMU) Elac2	219	DSSAGANRKANGRPDSLVAVAVCKLHLKGNFLVLKAKELGIPVGTAAIAPITIAAVKDGKSTT·YEGREHIAAEECTP.....PDPLVEIIVVECP·DEGF
(CEL) CE16965	238	.....KNV·KVNVDIAELIEMKBAARRIDTNKLMELKVP·K·GP·..LIGLKSGBAVTLPDGRTHQPDQVFESSDKVEGDKPLL·LWTECTEDH·
(ATH) gi6850339	203	.....LSVVVVCCLPEILGKFDLEKAK·VGVKPGPYSRLOSSES VKS·DERDITVHPSDWMP·...SLPGPIVLLVDCPTESHA
(SCE) YKR079C	181	.....VELPDLDAVENVSTNVEISPSVRGKFKVEAIKLGVP·K·GP·..LFAKLTGQHTLDNGIIVTPREQULENER.....HFAKVLILDIP·DDLY
(HSA) ELAC2	317	IQPIECENATFORQCKADAPVAL.....VWHMAPASVLVDSNQW MERFGPDQ·ELVNMENCASVNL·RSHKIQTQLNLIHPDIFELL.....
(MMU) Elac2	313	ILPIECENDTFKRYQAEADAPVAL.....AVHIAPEBVLIDSRNQW MERFGPDQ·ELIINENCPSVNL·RSHKIQTQLSLIHPDIFELL.....
(CEL) CE16965	322	VKALIDSSSIQPFNGEKQLDY·...VWHISDDAVINTPTVRHL MEKLNPSITHELLNGGNPVI PAVESVYKHTRLRSIAPSLEPAL.....
(ATH) gi6850339	280	ABIEFSLKLSIESYSSPDEQITGAKFVNCIHLSPSSVTSPTVQSW MKKFEHL·TQ·HILAGHORFLPLLIVSHQKT....VRKNWAPFLKASSRIAA
(SCE) YKR079C	266	LNAAFEVK·FKDNDCA·ELGMVYVFLGDEVTINDNLFAPIDIEKNVGVKUNH MISENKISNTISFPGSALTTLKKAQV·NNYNLEKTRDVFESKDF

FIG. 6A-1

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(HSA) ELAC2	401	...TSPRCKKEGPTLSVPMVQGECLLKYLPRRRWQR.....DAITCNPEEFIVEAL...QLPNFQSQVQYRRSAQDG.	
(MMU) Elac2	397	...TSFYSKEEGSTISVPTVRGECLLKYLPRKRWQR.....DTLDCNDEPIABAL...ELPSFQESVEYRKNVQEN.	
(CEL) CE16965	407	...HPIDWSGIITONEELSORDDQFIRV-APMQRYWR.....RGA..SPPEEPIVNNLLAAEPELSDXAK.ELIKEYOK..	
(ATH) gi6850339	374	RINYLCPQFFPAPGFWPSQLTDSHIDPPSNKP-NLRPVAIRGIDRSCIPAPLTSSVVDLLSEIPEIKDKSEIKQFNNKQHNKTIIEKWLSECNT	
(SCE) YKR079C	362	YDRFDTPLSRGTSMKCSQEEPLNTLLEKDNHIFSONKTVTPEPRMNEBPMKCNINGEVADFSWQEIPEE-HVKPPL-EPPLADVD-TVINNQLHVDN..	
			1641 insG
(HSA) ELAC2	471	..PAPAEKRSQYPEIIF.LGTGSAIPMKIRNVSAITLWNISP.....DTSLLDDCGEGTFFGQLCRHYGQD.VDRWLGTLAAVFWVSHLHDDHHTCGLPSI	Δ541 disruption
(MMU) Elac2	467	..PAPAEKRSQYPEIIV.LGTGSAIPMEIRNVSSITLWNLSP.....DKSWLLDCGEGTFFGQLCRHWGQO-IDRWLCSLTAVFWVSHLHDDHHTCGLLNI	
(CEL) CE16965	475	..LEKENKMDCEFPKLTFFGTSSAVPSKYRNVTG.VLVRASE.....NSAILIDVGEGETYGGMRVFGEDGCKQLLVNLCNVLITTHAQDHQHMNGLYTI	
(ATH) gi6850339	473	VLPNCLEKIRRDDMEIVILGTGSSQPSKRYRNVSATPFDLFS.....RGSLLDDCGEGTFFGQLKRRYGLDGADENRKLRCIWIWISHIHADHHTCGLARI	
(SCE) YKR079C	456	FNNSAEKKKHVEIIT..LGTGSAIPSKYRNVSITLWKVPFTDADGNTINRNIMLDACENTLGTIHRMESQLAVKSHQDCLKMEYLSHLHDDHHLCGLISV	
(HSA) ELAC1	1	MSMDVTF.LGTGAAYPSPTGASAVVRCE.....GECWLFDCGEGTQTQD.....MKSQKAGRI TKLITITTHLHGGHFFFGLPGL	
(Es c) elac	1	MKRDELMLIF.LGTSAQVPTRTNNTA-TILNLQHPF...QSGLMLFDGEGTQHQL.....LHTAPNPKLQKXIFISHLHGGHFLFGLPGL	
(Syn_sp) gi2500943	1	MEITP.LGTSSGVPTRNRNVSS-TIALRLPQ.....RAELMLFDGEGTQHOF.....LRSEVMISQLTRITITTHLHGGHIFGLMGL	
(Me t) gi2622965	1	MNEVTF.LGTSSAVPSKXNNEITS-TIALRIP.....GEIIFLFDGEGTQROM.....ALAGISPKNUTRITITTHLHGGHILGLIPOM	

FIG. 6A-2



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(HSA)ELAC2	559	LLQPERALASLGKPLHPLVWAPNQLKAWLQYHNQCQEVLLHISMIPAKCLQEGAEISSPAVERLISSLRTC	.....
(MMU)Elac2	555	LLQREHALASLGKPPQLVWAPNQLKAWLQYHNQCQEVLLHISMIPAKCLQEGAEVSNITLERLISLLETCT	.....
(CEL)CE16965	565	IARRKEAFESLGAPEPLVWAPNQLKAWLQYHNQCQEVLLHISMIPAKCLQEGAEVSNITLERLISLLETCT	.....
(ATH)gi6850339	564	LAL..RSKLLKGVTHPEVIVWGPPLKREDDAYQRLDMEFDCRSTATSWASLESGBAEGSLFTQ..GSPMQSVFKRSDISMNSSVLLC..LK	.....
(SCB)YKR079C	554	L..NEWYKYNKDDETSIVVWTPQVYKFFVNEML..VLENKEILKRIKYSISCEHFINDSFVRMOTQSVPLAFNEILKENSNOESNRKLELDRDSSRYDVD	.....
(HSA)ELAC1	75	LC..TISLQSGSMVSKQIEIYGPVGLRDFIWRMTMELSHTELVFHYV..HELVPADQCPAEELKEFAHVRNADS	.....
(Es c)elac	83	L.....CSRNSGIIQLTIYGPQCIREFNETAL	.....
(Syn sp)gi2500943	75	L.....ASSGLAGSGQIEIYGPGLGDLKACC	.....
(Me t)gi2622965	74	L.....QSMGPRGRREPLDIYGPGLHELHECTM	.....
(HSA)ELAC2	633	.....DUEEFQTCIVRHCKH..AFGCALVHT	.....
(MMU)Elac2	629	.....DUEEFQTCIVRHCKH..AFGCALVHS	.....
(CEL)CE16965	650	SSSPDKKAWKLDLKAQVHHTRMANGFVMRV	.....
(ATH)gi6850339	657	NLKKVLSBIGLNDLISFPVWHCPQAYGWIKMAER	.....
(SCB)YKR079C	651	LIRQVYEDLSIEYFQTCRAIHCDW..ATNSNITFR	.....
(HSA)ELAC1	163	NSYLLFDDEQV..WKAPRTHRIIPSGFSSVVEKKRPGKLNQKLDLGVPPGPAYGKLNKNGISVVLNGVTISPQDVLKAPIVGRKICILGDCSG	.....
(Es c)elac	130	..GEIIDDGLRK..WTAYDEHPLECYGRIEEDHKPGALNAQALKAAGVPPGLFQELKAGKTIILEDGRQINGADYLAAPVPGKALAIFFDTCDE	.....
(Syn sp)gi2500943	122	N..GLIYEDKDFQ..VHCGLLKRIIPAGVRVVEKQRPGRNVEQABALGIPFGPIYGQLKQKTVTLEDGRRIRRGODLCEPPEPGRFVYCTDTVF	.....
(Me t)gi2622965	121	G..TVV..EEDDYR..VTSAPASUSVFNLANCFEEXKRRP..FLREKAIALGLKPGAFAGKLRGIPVRVG	.....

FIG. 6B-1

**FIG. 6B-2**

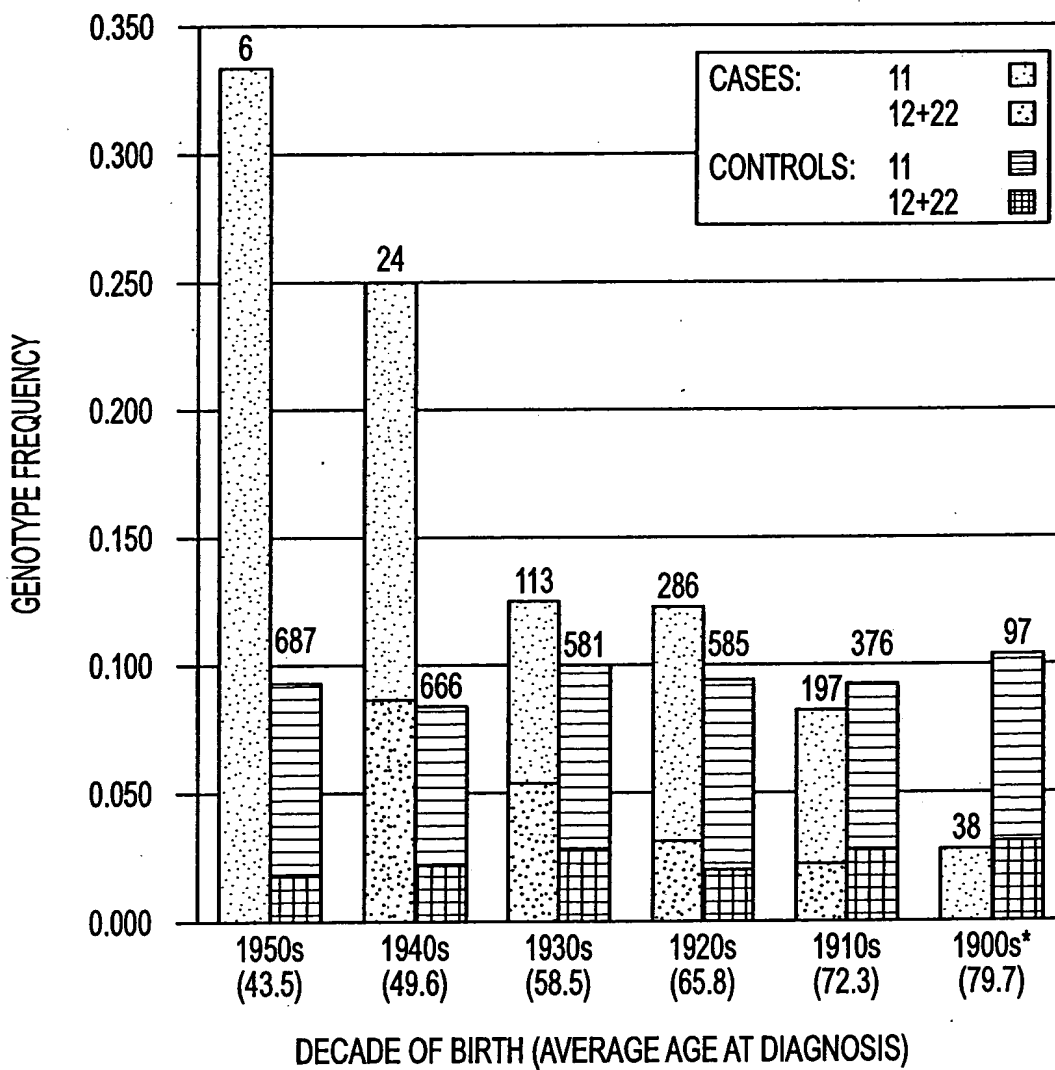


FIG. 7

	OBSERVED	
	CASES	CONTROLS
00, 01, 02	372	139
11, 12, 22	57 (13.3%)	9 (6.1%)

00, 01, 11	387	143
02, 12, 22	42 (9.8%)	5 (3.4%)

00, 01	347	137
02, 11, 12, 22	82 (19.1%)	11 (7.4%)

## 1920s - 1950s CASES VS. PEDIGREE UNAFFECTEDS

00, 01, 02	372	2151
11, 12, 22	57 (13.3%)	220 (9.3%)

00, 01, 02	372	2151
11	40 (9.3%)	170 (7.2%)
12, 22	17 (4.0%)	50 (2.1%)

FIG. 8

FIG. 9-1

CPSF73 family	
(HSA) CPSF73	1 MSAPAEESDQILRPLGAGQEVGRSCILLEPKGRKIMLDCGIIHPC · LEGMDALPY · IDLIDPAEIDLLISHFHLDCGALPWFLOKT
(ATH) gi6751699	1 MASSSTSLKRRQPISRDGDQIIVTPLGAGSEVGRSCVMSFGKNIILDCGIIHPC · YSGMAALPY · FDEIDPSSIDVLLITRPHIDHAASLPYRLEKT
(SCE) YSH1	1 MERTNTTTFKPFSLGGSNEVGRSCHILQYKGTWMDAGIHPA · YQGLASLPF · YDEFDLSKWDILLISHFHLDCGALPWFLOKT
(Syn sp) gi2496795	1 MTGSVPTQCAAFANISLPGVGRPD · GGICLHLGCPYRILDCGLEB · · · · · DPCTVDLVCCSHAHRDHIGLWQFHQPF
(Me_t) gi2622312	161 ILQQLGNRIHQKPKVDND · WARDTA · MGGPREVGRSCLYLQTPNSRMVLD · CGVNVAGDDKNSPYLNVPFETLDS · DAVIITTHAHLDCGELPYL · YHY
PS02 family	
(HSA) ha3611	651 KRSDHLIN · TESEAVNLSKVMETKSA · HGGLQGNKAKIPESNVGGRKATCPFKAKIPGTGTVDAPQVGVVEGCTANFLTRFHSDEHAGLSKHPTFP
(ATH) gi2979557	350 TANKLITREPPGQATGCTKIRTAAPKPAEKSPSDSSRAVRNNGNKGSKVIPHNMICPGTPPRVDAFKYLTRD · CCHMFLTRFHLDCGALPWFLOKT
(SCE) PS02	165 HDCTCIGSDPSNMGTGPKNIIRSFISNPSPAKTKRDIATSKKPRVKLVLPSPKIIKFNNGHEIVVDGPNYKASET · GYFLSHFHSDEHAGLSKHPTFP
ELAC2 family	
(HSA) ELAC2	481 · · · · · PEIIFLGTSAPKIRINVSATLVNISP · · · · · DTSLLDGEGGTGQL · CRHYGDQ · VDRVLGTDAVEN · SLSHADHHTGLPSILLOK
(ATH) gi6850339	485 · · · · · MEIVILGTSSQSKYRNVSALFIDFS · · · · · RGSLLDGCGETGQL · KRRVGLDGADEAVRKLRCIMISHHADHHTGLARILAIR
(SCE) YKR079C	466 · · · · · VEIITLGTGSAIPSKYRNVSATLVNISP · · · · · NRNIMLDAGENTLGTI · HRNFSQALAVSIFQDLKINILSHHADHHTGLISVLNEW
CPSF73 family	
(HSA) CPSF73	148 · · · · · GIKFWCYHAGHVLGAMFMIRIA · · · · · GVKLLVTCDFPS · · · · · RQEDRHLMAAEIPNIK · PDILIIESTTGTHI · HEKREEREARFCNTVH
(ATH) gi6751699	158 · · · · · GIKFWCYHAGHVLGAMFMIRIA · · · · · GVRILYTCDFPS · · · · · REEDRHLMAAEIPNIK · PDILIIESTTGTHI · HEKREEREARFCNTVH
(SCE) YSH1	153 · · · · · GIKFTAFHAGHVLGAMFMIRIA · · · · · GVRILYTCDFPS · · · · · REEDRHLMAAEIPNIK · PDILIIESTTGTHI · HEKREEREARFCNTVH
(Syn sp) gi2496795	125 · · · · · GUTVELLPAGHLPAGHLLILEYHNG · · · · · DRLYRVITGTDY · CLSHLQLDVGLALTPRLGK · PDVILLEGHGNRR · LPHRRQERQFQIAIE
(Me_t) gi2622312	319 · · · · · DURLTLHNAGHILGSAWAHLHIG · · · · · DGQNMVYTCDFK · · · · · YEQSRLLLEAANRPR · IETAVMESTYGGHEDVQPSNRRAEKLVTYI
PS02 family	
(HSA) ha3611	783 · · · · · GVKWLLDANHCPCGAWILFVLP · · · · · NGTVILHTGDFRADPSNERSLLADOK · · · · · VHMVLDITVCSPEYTFPSQOEVRPAINTAF
(ATH) gi2979557	484 · · · · · GUDVTCFDANHCPCGAWILFVLP · · · · · NGXAVLHTGDFRADPSNERSLLADOK · · · · · ISSULDDITVCSPEYTFPSQOEVRPAINTAF
(SCE) PS02	308 · · · · · TGSWVTLNHCPCGAWILFVLP · · · · · NSVDKPIRQILHTGDFRADPSNERSLLADOK · · · · · TQVILDDITVCSPEYTFPSQOEVRPAINTAF

FIG. 9-1

FIG. 9-2

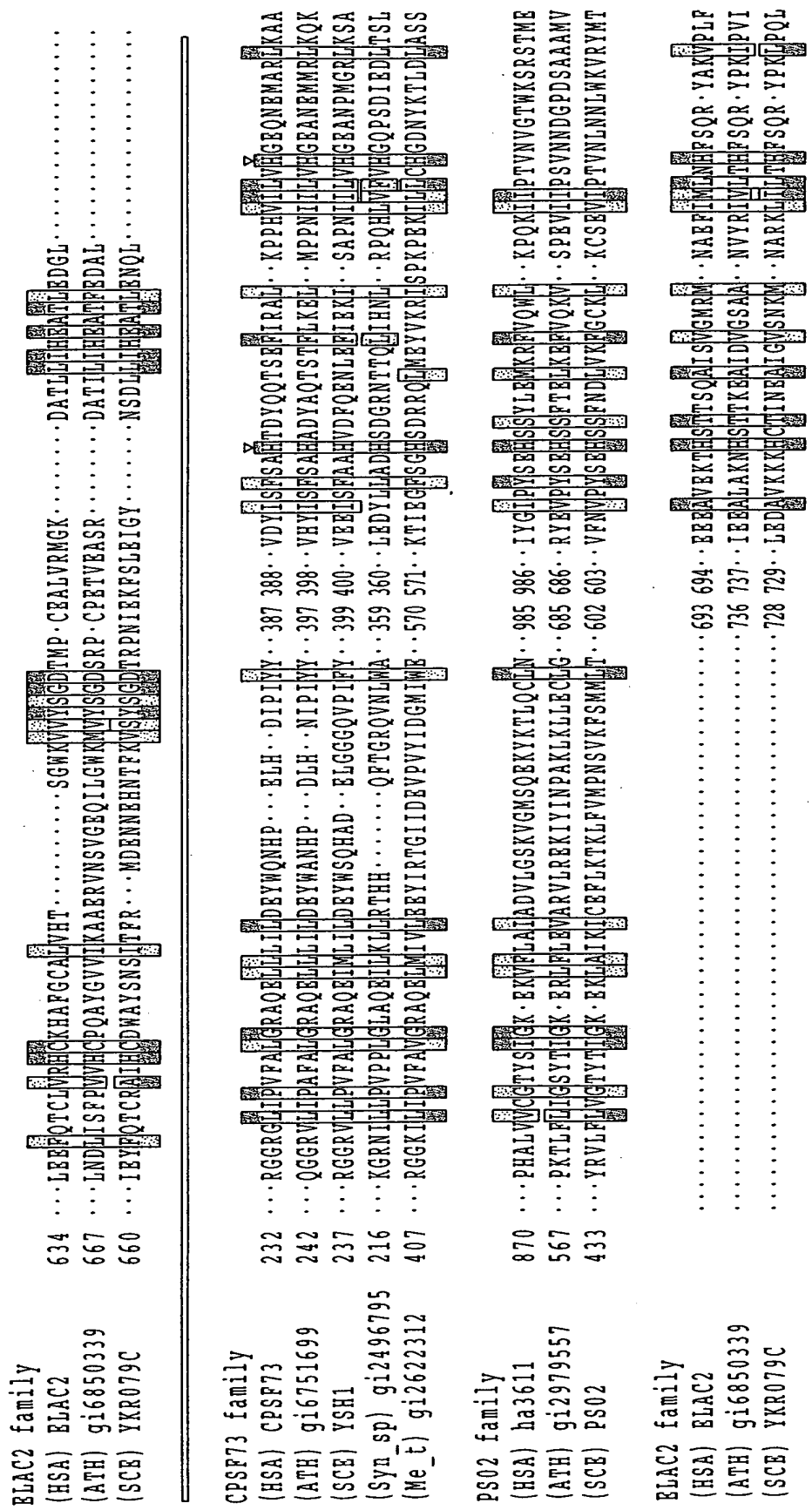


FIG. 9-2

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	(HSA) ELAC2			(MMU) Elac2			(CEL) CE16965			(ATH) gi6850339			(SCE) YKR079C		
	%ID	%SIM	%GAP	%ID	%SIM	%GAP	%ID	%SIM	%GAP	%ID	%SIM	%GAP	%ID	%SIM	%GAP
(HSA) ELAC2	100.0	100.0	0.0	-	-	-	-	-	-	-	-	-	-	-	-
(MMU) Elac2	81.6	88.0	1.8	100.0	100.0	0.0	-	-	-	-	-	-	-	-	-
(CEL) CE16965	24.2	43.0	14.0	24.6	44.0	15.7	100.0	100.0	0.0	-	-	-	-	-	-
(ATH) gi6850339	25.6	47.0	23.5	25.4	46.0	25.0	21.0	44.0	21.1	100.0	100.0	0.0	-	-	-
(SCE) YKR079C	21.8	41.0	20.8	21.7	43.0	21.4	18.2	43.0	21.4	21.8	41.0	16.3	100.0	100.0	0.0

FIG. 10

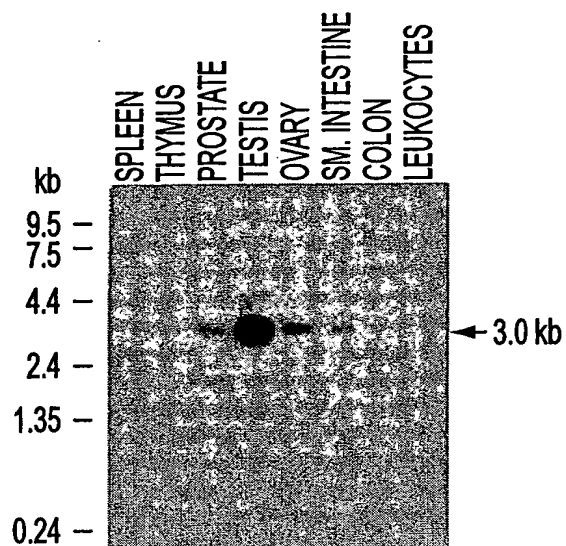
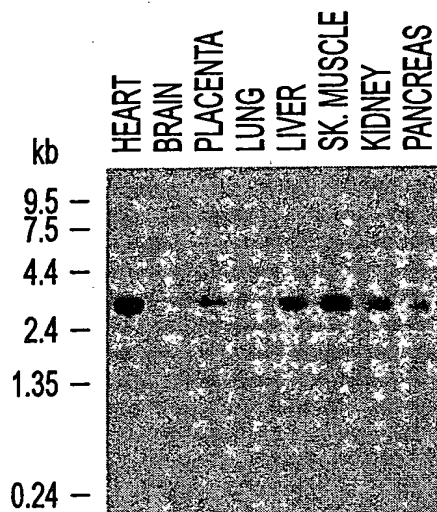




FIG. 12

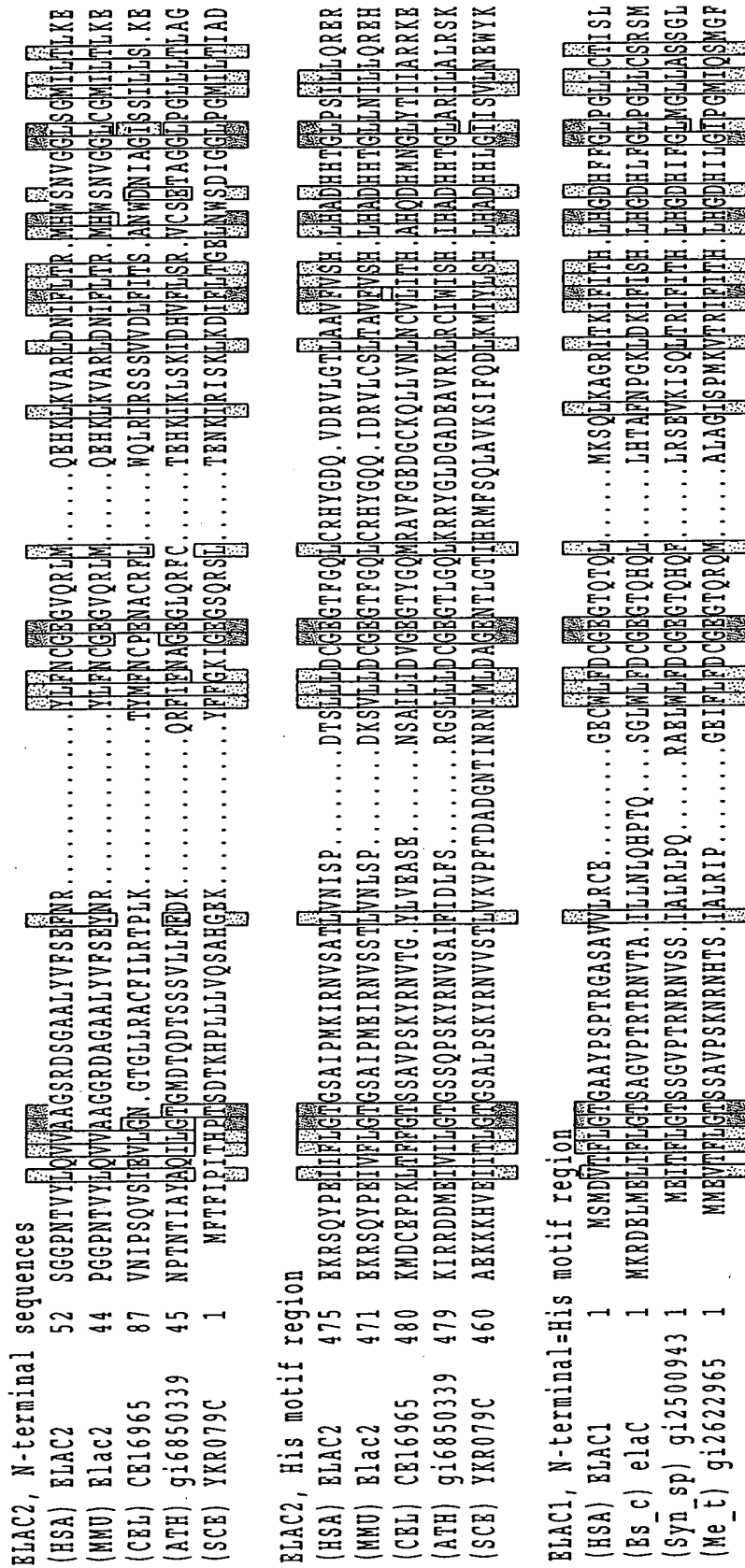
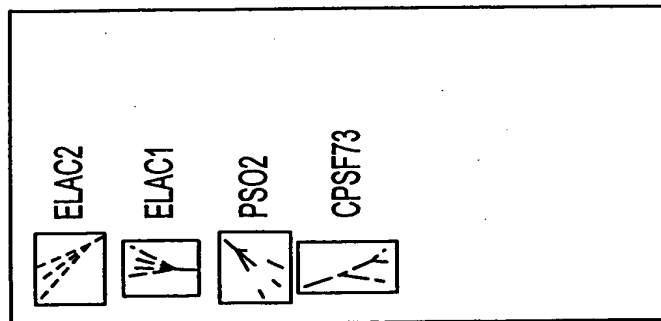


FIG. 12



Eukaryota  
Eubacteria  
Archaea

**FIG. 13**